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OM protein - protein search, using sw model

Run on:

December 19, 2002, 15:00:53 ; Search time 18 seconds

2143.388 Million cell updates/sec

Title: US-08-813-323B-1

Perfect score: 2994

Sequence: 1 MESSKKMDAAGTLQPNPPLK..... IKDDDTIFKVIVDSDLDPD 567

Scoring table: BLOSUM62

GapOp 10.0 , GapExt 0.5

Searched: 245176 seqs, 68044064 residues

Total number of hits satisfying chosen parameters: 245176

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending_Patents_AA_New:*

1: /cgn2_6/ptodata/1/paa/US06_NEWCOMB.pep:*

2: /cgn2_6/ptodata/1/paa/US07_NEWCOMB.pep:*

3: /cgn2_6/ptodata/1/paa/US09_NEWCOMB.pep:*

4: /cgn2_6/ptodata/1/paa/US10_NEWCOMB.pep:*

5: /cgn2_6/ptodata/1/paa/US10_NEWCOMB.pep:*

6: /cgn2_6/ptodata/1/paa/US10_NEWCOMB.pep:*

7: /cgn2_6/ptodata/1/paa/US06_NEWCOMB.pep:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID

Description

1: 837.5 28.0 501 6 US-10-283-500-4

Sequence 4, Appl 1

Sequence 53797, A

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending_Patents_AA_New:*

1: /cgn2_6/ptodata/1/paa/US06_NEWCOMB.pep:*

2: /cgn2_6/ptodata/1/paa/US07_NEWCOMB.pep:*

3: /cgn2_6/ptodata/1/paa/US09_NEWCOMB.pep:*

4: /cgn2_6/ptodata/1/paa/US10_NEWCOMB.pep:*

5: /cgn2_6/ptodata/1/paa/US10_NEWCOMB.pep:*

6: /cgn2_6/ptodata/1/paa/US10_NEWCOMB.pep:*

7: /cgn2_6/ptodata/1/paa/US06_NEWCOMB.pep:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT	1
US-10-283-500-4	
Sequence 4, Application US/10283500	
GENERAL INFORMATION:	
APPLICANT: Goeddel, David V.	
Rothe, Mike	
TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated Factors	
NUMBER OF SEQUENCES: 59	
CORRESPONDENCE ADDRESS:	
ADDRESSEE: Genentech, Inc.	
STREET: 460 Point San Bruno Blvd	
CITY: South San Francisco	
STATE: California	
ZIP: 94080	
COMPUTER READABLE FORM:	
COMPUTER: IBM PC compatible	
OPERATING SYSTEM: MS-DOS	
SOFTWARE: WinPatin (Genentech)	
CURRENT APPLICATION DATA:	
APPLICATION NUMBER: US/10-283-500	
FILING DATE: 30-Oct-2002	
CLASSIFICATION: <Unknown>	
PRIOR APPLICATION DATA:	
APPLICATION NUMBER: US/08/779,599	
FILING DATE: 07-Jan-1997	
ATTORNEY/AGENT INFORMATION:	
NAME: Dinger, Ginger R.	
REGISTRATION NUMBER: 33,055	
REFERENCE/DOCKET NUMBER: P0897C2	
TELECOMMUNICATION INFORMATION:	
TELEPHONE: 415/952-3216	
TELEX: 910/371-9881	
INFORMATION FOR SEQ ID NO: 4:	
SEQUENCE CHARACTERISTICS:	
LENGTH: 501 amino acids	
TYPE: Amino Acid	
TOPOLOGY: Linear	
SEQUENCE DESCRIPTION: SEQ ID NO: 4:	
US-10-283-500-4	

Query Match 28.0%; Score 837.5; DB 6; Length 501; Best Local Similarity 33.5%; Pred. No. 4.7e-71; Matches 194; Conservative 88; Mismatches 198; Indels 99; Gaps 16; Sequence 85180, A

Sequence 85182, A

Sequence 85183, A

Sequence 85184, A

Sequence 85185, A

Sequence 85186, A

Sequence 85187, A

Sequence 85188, A

Sequence 85189, A

Sequence 85190, A

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Sequence 85208, A

Sequence 85209, A

Sequence 85210, A

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Sequence 85212, A

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Sequence 85214, A

Sequence 85215, A

Sequence 85216, A

Sequence 85217, A

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Sequence 85249, A

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Sequence 85257, A

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Sequence 85495, A

Sequence 85496, A

Sequence 85497, A

Sequence 85498, A

Sequence 85499, A

Sequence 85500, A

RESULT 2
 US-09-724-676-53797
 Sequence 53797, Application US/09724676
 ; GENERAL INFORMATION:
 ; APPLICANT: Compugen LTD
 ; TITLE OR INVENTION: Variants of alternative splicing
 ; FILE REFERENCE: 129181.4 Compugen
 ; CURRENT APPLICATION NUMBER: US/09/724, 676
 ; CURRENT FILING DATE: 2000-11-28
 ; NUMBER OF SEQ ID NOS: 97222
 ; SEQ ID NO 53797
 ; LENGTH: 519
 ; SOFTWARE: Patentin version 3.2
 ; SEQ ID NO 53797
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-724-676-53797

Query Match 23 0% Score 688.5; DB 5; Length 519;
 Best Local Similarity 31.9%; Pred. No. 6.6e-57; Gaps 19;
 Matches 169; Conservative 89; Mismatches 174; Indels 97;

QY 66 ECCHRFCECSMAALLSSSSPKCTAC---QESTI--KDKVVKDNCKRETLALQYTC 116
 QY :|||:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 48 QCCHRYSFCFLSISLSSGPNQACACTYEGLYEEGISILESSAFAFPDNARKGVESL 107
 Db 117 RNSGRGCACBQLTGHLLVHLKNQCFEELPCIRADKEKVLKDLRDHYEKAC 176
 QY :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 108 PND--GCTWKGTKEYESCHEICPFLTEC--PACKGLYRLSEKEHHTHQECPKRSUC 163
 QY :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 177 SHRSQVNMVKLOKHEDDCPCVVSCPHKSQVTLSELSEAHSECWVAPSTCSFKY 236
 QY :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 164 QHCRCPSHVDLVEHYEV--CPKPLTC--DGCKKKIPREKFQDHVRACKRVLGRFTV 221
 QY :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 237 GCVFGTNQIKAHQAASSAVOHVNLLKEWSNLSLEKK-----LQNESEVKNS 286
 QY :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 222 GCSMEVNETMLQDLELQRLLREHALL--LSSLEAQASPGNLQVQPELQLRQCQLEQK- 278
 QY 287 IOLHNQICSFIEIEROKEMLRNNESKILHQLRVIDSQAEKLKEDETRPPRQNWEA 346
 QY :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 279 LATFNTIVCVLNREVER-----VAVTAEACSRQHRLQD----- 312
 Db 347 DMSKSSVSLQNRVTELESVDSKAQAAARTNGLESQLSRHDQTLSVHDTLADMRLFQ 406
 QY :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 313 -----KIEALSLNKVQOLE-----RSIGLKDLMADLQKVS 343
 QY 407 VLETASYNGVLIWKIRDYKRRKQAVMGKTLISLSSQPFYTFGYKMACRYLNGGMK 466
 QY :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 344 ELEVSYIDGFIFWKISDFRKFRKRQBAVAGRTPAFSPARFTSYRGYKMCRLVYLNGDGR 403
 QY 467 GTHLSSLFFVIRNGEYDALLPPWPKQVTMLMDGSSSRHLGDAFKDPNNSFFKPTGE 526
 QY :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 404 GTHLSSLFFVWKKGPNDALLOWPPNOKVTLMLDHN-NRREHVIDAFRPDVTSFSFORPVSD 462
 QY 527 ANTIASCSCPVFAQTVLE-NGTYIKDTITKVTDTSDL 564
 QY :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 463 MNIASGCPPLFCPVSKMEEAKNSYVRDDAIKAIVDLTGL 501

RESULT 3
 US-09-724-676A-53797
 Sequence 53797, Application US/09724676A
 ; GENERAL INFORMATION:
 ; APPLICANT: Compugen LTD
 ; TITLE OF INVENTION: Variants of alternative splicing
 ; FILE REFERENCE: 129181.4 Compugen
 ; CURRENT APPLICATION NUMBER: US/09/724, 676A
 ; CURRENT FILING DATE: 2000-11-28
 ; NUMBER OF SEQ ID NOS: 97222
 ; SOFTWARE: Patentin version 3.2
 ; SEQ ID NO 53797
 ; LENGTH: 519
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-724-676A-53797

Query Match 23 0% Score 688.5; DB 5; Length 519;
 Best Local Similarity 31.9%; Pred. No. 6.6e-57; Gaps 19;
 Matches 169; Conservative 89; Mismatches 174; Indels 97;

QY 62 PKQTEGHRFCECSMAALLSSSSPKCTAC--QESTIKDV-----FKDNCKRETLAL 112
 QY :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 62 PFOAQCGHRYCSFCFLSISLSSGPNQACACTYEGLYEEGISILESSAFAFPDNARKGVESL 121
 QY 113 QVYCRNEGRGCAEQLTGHLLVHLKNQCFEELPCIRAD--CKEKVLRKDLRDHYEKAC 169
 QY :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 122 PAVCPSD--GCTWKGTKEY -----ESCHEGRCPLMLTCPACKGLVRLGEKERHEC 174
 QY 170 KYREATCSHCKSQVPMVKLOKHEDDCPCVVSCPHKSQVTLSELSEAHSECWAPS 229
 QY :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 175 PERSLSRCRCCPAGDVKAHEV--CPKPLTC--DGCKKKIPREKFQDHVKTCGRV 232
 QY 230 TOSFKRYGV--FQGNAQTKAHEASSAVOHVNLLKEWSNLSLEKK-----VSLIQ 277
 QY :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 233 PCRFHAIGCLETVEGERKQO--EHEYOWLREHLLM--LSSLEAKPLGDOSHAGSELLQ 288
 QY 278 N-ESVERNKSTIOSLHNQICSFIEIEROKEMLRNNESKILHQLRVIDSQAEKLKEDE 336
 QY :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 289 RCESLREKTA--TFENIVCVLNREVER-----VAMTAEACS----- 322
 QY 337 RPFRQNWEADSMKSSVSLQNRVTELESVDSKAQAAARTNGLESQLSRHDQTLSVHDI 396
 QY :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 397 RLADMDFRQVLETASYNGVLIWKIRDYKRRKQAVMGKTLISLSSQPFYTFGYKMKAR 456
 QY :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 352 AMADLQKVRPFOAQCGHRYCSFCFLSILRKLOQEAVGRIPAISSPAFTSYRGYKMCRL 411
 QY 230 TCSFKRYGV--FQGNTQOJKAHEASSAVOHVNLLKEWSNLSLEKK-----VSLIQ 277

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RESULT 4
US-03-724-676-84446
; Sequence 84446, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 84446
; LENGTH: 308
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-03-724-676-84446

```

Best Matches	Local Similarity	Pred.	No.	1.2e-56;	Mismatches	Indels	Gaps
QY	271	KRVSSLQNEESVEVKNSISSLHNOICSFETEIEROKEMLRNNESKILHQRQVPSQAEKIK	330				
Db	13	KOISDLHKSLQEKSILQQLAETIKKLEKEFKOFQAOLFGKNGSFLPNIO-VFASHIDKSA	71				
QY	331	ELDKEIRPF-----RDNWEEADSMKSVESLQNRVTELESVOKSAGQDARNTGLLESQI	384				
Db	72	WLEAQVHOLLQMVNQONQKFDRPLMVEADTVQKRITLEND-----ORLAVLEEB	124				
QY	385	SRDQTLTSWHDRLADMDRLRFQLETASYNLWIKRDYKRRKOEAVGKTSLSYDQP	444				
Db	125	NKRDTHLNIIKHAQSKNERFKLEGTCYNGKJLJWKVTDYKMKRREAGDHTVSISFSQSF	184				
QY	445	YTGFGYKMCARYVYLNGDGMGKGTHLSLFPVIMRGEDYDALLPNPWFQKVYTLMDQGSSR	504				
Db	185	YTSRCGIRLCARAYLNGDGSGRGSHLSLYFVVMERGEFDSSLQWPFRQRTMLLDQ-SCK	243				
QY	505	RHLGDAKRPDPSSSEKFPTGEMNIASGCCPVPVFAQTVLN--GTYIKDTTIFKIVDWS	562				
Db	244	KNIMETFRPDPNSSFKRDPGENMIASGCCPVPFVHSVLENAKNAVYIKDDTFLRKVADLT	303				
QY	563	DIPD 566					

RESULT 7

US-09-724-676A-53795

Sequence 53795, Application US/09/724676A

GENERAL INFORMATION:

APPLICANT: Rothe, Mike

GENERAL INFORMATION:

APPLICANT: Compugen LTD

TITLE OF INVENTION: Variants of alternative splicing

FILE REFERENCE: 129181-4 Compugen

CURRENT APPLICATION NUMBER: US/09/724, 676A

CURRENT FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222

SOFTWARE: Patentin version 3.2

SEQ ID NO 53796

LENGTH: 536

TYPE: PRT

ORGANISM: HOMO sapiens

US-09-724-676A-53796

Query Match 21.8%; Score 652.5; DB 5; Length 536; Best Local Similarity 31.2%; Pred. No. 1.8e-53; Matches 161; Conservative 88; Mismatches 170; Indels 97; Gaps 19;

QY 62 PRQTECGHRCTCESMAALISSSSPKCTAC-QESTIKDV-----FKNCCREILAU 112

Db 62 PFOAQCGHRCFCSFLASIILSSGPQNCAACVHEGYIEEGISILESSAFFPNAARKGVESI 121

QY 113 QVYCERNERGRCRCAEQLTGLIGHVLWHLKNECQEEPLCLRAD--ČKEKVLKDRDHEVKAC 169

Db 122 PAVCPSD--GCTWKGPKEY --- E SCHGRCPLMLTEC PACKGLVRLGEKERHLEH C 174

QY 170 KYREATCSHOKSQVPMIKLOKHEDTCPVCVWSCHPKCSVQTLRSLSLSEAHSLBCVNAES 229

Db 175 PERSLSRHCIRRAPCAGDVKAHHEV-CPRPLTC-DGCCKKTREKFQDHVKCCKCRV 232

QY 230 TCSFKRYGYC---FOGTNQTKAHEASSAVYOHVNLUKEWSLKK-----VSLLQ 277

Db 233 PCRFHAIKGCTEVGEKQQ---EHEVQWLREBLAML---LSSVLEAKPLLGDSOSHAGSELIQ 288

QY 278 N-ESVEKNIKSQIQLNOTCSFEIETRQEKMRLRNNESKITHLQRVIDSOAELKELDEI 336

Db 289 RCESELKTTA-TFENIVCVLNREVER-----VAMTAEACS----- 322

QY 337 RPFRQWEADSMKSVESI-QNRVTELESVDKSAGQAARTNGLLESQSLRHDQTLVHDI 396

Db 323 ---ROHRLDOD----KIEAALSKVQOLE-----RSIGKL 351

QY 397 RLADMRLRFOVLETASYNGVLIWKIRDYKRKRQEAVMGKILSLSQPFYTGYEGYKMCAR 456

Db 352 AMADIEQKVPPQACQGHRCFCSFLASIILRKLOBAVAGIPIATSPAFTRSYCCKMCLR 411

QY 457 WYLNGDGMSGKTHLSLFFVIMRGEXDALLFWPFKOKVTMLMDQGSSRRHLGDAFKPDPN 516

Db 412 IYLNQDGTTGTHLSLFFVWKGPNNDALLWRPNOKVTLMDQ-NNREHVIDAFRPDVT 470

QY 517 SSSKKPTGEMNIASGCPWPVVAQTYLE-NGTYIKDD 551

Db 471 SSSFORPVNDMNIASGCPWPVSKMEAKNSYVRDD 506

Query Match 21.4%; Score 640; DB 6; Length 409; Best Local Similarity 35.5%; Pred. No. 1.9e-52; Matches 162; Conservative 72; Mismatches 136; Indels 86; Gaps 15;

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 409 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-10-283-500-2

Query Match 21.4%; Score 640; DB 6; Length 409; Best Local Similarity 35.5%; Pred. No. 1.9e-52; Matches 162; Conservative 72; Mismatches 136; Indels 86; Gaps 15;

QY 137 KNECOFFEELPCPLRADCOKERVKVLKDLRDRDHEVKACYRERATCSHCKSQVPMIKLOKHEDTCP 196

Db 9 ENERQF-- GCPPAPCQD-----PSPRPRVLCCTACLS-----NURDEDRIC 48

QY 197 PCVUVSPCPHKCSVQTLRSLSLSAHSLUSECVNAPSTCFSKFRYGVCFQGTOQOKIAHEASSAV 256

Db 49 PKCRADNLHPVSPGSPLTQE-KVH-SDVAEAEIMCPFAGVGCSFRKGSPSOMSHEATSQS 106

QY 257 QHVML---LKWSNS-----LEKKVSLQNESVEKNIKSQIQLHQICSEFEIETI 301

Db 107 SHLYLILAVLKEWKSSPGNSLGSAPMALBNLSELO-----LQAVEAENGDELVD 157

QY 302 EROKEMLRNNESKILHQLRVIDSOEK-LKELDEKEIRRPRQWNWEADSMKSVESLQNRV 360

Db 158 YRACPCESEELAOHLHVK-----EKLQALEEKLV-----ANTIVALKIE 200

QY 361 TELESVDKSAGQAARTNGLLESQSLRHDQTLVHDI 408

Db 201 VE-----ASHLAALAASTHQSOQDRREHILSLEORVVELQQTIAQDKQVLGKLEHSRIM 253

QY 409 ETASYNGVLIWKIRDYKRKRQEAVMGKILSLSQPFYTGYEGYKMCARVYLNGDMGKGT 468

Db 254 EEAISDGTFLWKITNTVKRCHESVGRIVLSPAFVYATAKYGYKLCLRLYLNQSGKRT 313

QY 469 HLSLFFVIMRGEXDALLFWPFKOKVTMLMDQGSSRRHLGDAFKPDPNNSFRKPTGEMN 528

Db 314 HLSLFFVIMRGEXDALLFWPFKOKVTMLMDQGSSRRHLGDAFKPDPNNSFRKPTGEMN 372

GENERAL INFORMATION:

APPLICANT: Goeddel, David V.

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.

ADDRESS: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SUPERVISORY SYSTEM: WinPatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/283, 500

FILING DATE: 30-Oct-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/779, 599

FILING DATE: 07-Jan-1997

ATTORNEY/AGENT INFORMATION:

NAME: Dreger, Ginger R.

REGISTRATION NUMBER: 33,055

REFERENCE/DOCKET NUMBER: P0897C2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-3216

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 409 amino acids

TYPE: Amino Acid

QY 529 IASGCOPVFAQTVLEN--GTYIKDTIFIKVIVDTS 562 ; FILE REFERENCE: AMI0122BL
; CURRENT APPLICATION NUMBER: US/60/427,194
; CURRENT FILING DATE: 2002-11-19
; NUMBER OF SEQ ID NOS: 234
; SOFTWARE: PatentIn version 3.1

RESULT 9 ; SEQ ID NO: 89
US-60-423-586-89 ; LENGTH: 470
; Sequence 89, Application US/60423586
; GENERAL INFORMATION:
; APPLICANT: American Home Products Inc.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING SCHIZOPHRENIA
; FILE REFERENCE: AMI0128BL
; CURRENT APPLICATION NUMBER: US/60/423, 586
; CURRENT FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 234
; SOFTWARE: PatentIn version 3.1

QY ; SEQ ID NO: 89
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-60-423-586-89

Query Match 18.7%; Score 560.5; DB 7; Length 470;
Best Local Similarity 24.1%; Pred. No. 7.7e-45; Mismatches 24.1%;
Matches 142; Conservative 81; Indels 173; Gaps 12;

QY 37 GYKEFKVTKVEDVKYCEKCRVLICNPKO-TECGHRFCESCMALLSSSPKCTACQESII 95 ; Query Match 18.7%; Score 560.5; DB 7; Length 470;
CURRENT FILING DATE: 2002-11-05 ; Best Local Similarity 24.1%; Pred. No. 7.7e-45;
; NUMBER OF SEQ ID NOS: 234 ; Mismatches 173; Indels 193; Gaps 12;
; SOFTWARE: PatentIn version 3.1 ; Software: PatentIn version 3.1

Db 3 GFDYKFLEPKRRLCPLGKMRPQYQVSTGHRFCOTCQFELSEGVFKPEDIOLPD 62 ; SEQ ID NO: 89

QY 96 KDKYFKDNCKRETLALOYCRBGRGCABQLTGHLLWKNKNECOFEELPC----- 147 ; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-60-423-586-89

Db 63 YAKIYPDPLEVOVGLPPIRCIHSEEGCRWSGPLRHLOGHL NTCSFNVIPCPNRCPML 121

QY 148 -----LRAOCKE----- 18.7%; Score 560.5; DB 7; Length 470;
; Best Local Similarity 24.1%; Pred. No. 7.7e-45; Mismatches 24.1%;
; Matches 142; Conservative 81; Indels 193; Gaps 12;

Db 122 SRRDLPAHQDCPKRRLKEFGCDFSGEAYESHEGMCPQESVYENKGARMRMLA 181

QY 163 DHVREACKTREATCSHCKSOVPMILQKIEDTOPCUVVSCPHKSYCVTLLNSLSAIS 222

Db 182 OHATEBCPKTOPCYCTCERFVFTIQSIO----- 147

Db 241 DSCNTALVLCPPFDGCKHRCPKLAMARVEEVSKPHLM----- 281

QY 223 E-CVNAPSTCSFKRYGVCFQGTNOOKAHASSAVOHNLKELKNSLEKKVSLQNESV 281

Db 282 -----CA----- 18.7%; Score 560.5; DB 7; Length 470;
; Best Local Similarity 24.1%; Pred. No. 7.7e-45; Mismatches 24.1%;
; Matches 142; Conservative 81; Indels 173; Gaps 12;

QY 342 NWEADSMKSSVESLQRVTELESVDKSAGQAARTNGLLESQSLRSRHDOTLSVDIRLADM 401

Db 300 -----EELSV----- 18.7%; Score 560.5; DB 7; Length 470;
; Best Local Similarity 24.1%; Pred. No. 7.7e-45; Mismatches 24.1%;
; Matches 142; Conservative 81; Indels 173; Gaps 12;

QY 402 DLRFOVLETASYNGVLIWKIRDYKRRQEAVMGKTLISIQSOPFTGFGYKMCARVLYNG 461

Db 305 -----GSDGVLIWKGIGSYGRLOEAKPNLECFSPAFYTHKYGYKLOSAFLNG 354

QY 462 DCGMKGKTHLSLFFVIMRGYEDALLPPFKQVTLMLMDQ---SSRRHUGDAFPDPMS 517

Db 355 NGSGEGTHLSLFFVIRPGAFNLLPFPARRVTFSILDQSDPGLAKPQHVTETHPDPNW 414

QY 518 SSFPKKP----TGMNTIASCPVFAQTVLENGLTYIKDTIFIKVIVD 560

Db 415 KHFQKPETWRSGLDESSLGGFGYPKFISHODIRKRNVRDDAVFRAVE 463

RESULT 10 ; SEQ ID NO: 89
US-60-427-194-89 ; LENGTH: 470
; Sequence 89, Application US/60427194
; GENERAL INFORMATION:
; APPLICANT: American Home Products Inc.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING SCHIZOPHRENIA

RESULT 11 ; SEQ ID NO: 89
US-09-716-536-10 ; LENGTH: 470
; Sequence 10, Application US/09716536
; GENERAL INFORMATION:
; APPLICANT: Soo Young Lee
; TITLE OF INVENTION: Signal Transducer for the TNF Receptor
; TITLE OF INVENTION: Super Family and Uses Thereof
; FILE REFERENCE: 600-1-198CICON
; CURRENT APPLICATION NUMBER: US/09/716,536
; CURRENT FILING DATE: 2000-11-20
; PRIORITY NUMBER: 60/042,293
; PRIOR FILING DATE: 1997-04-01
; PRIORITY NUMBER: 60/042,747
; PRIORITY FILING DATE: 1997-04-07
; PRIORITY APPLICATION NUMBER: 08/834,903
; PRIORITY FILING DATE: 1997-04-07

Qy 443 PFTYGYFGYKMCARVYLNGDMGKGT 468
 : | : | : | : | : | : | : | : | : | : |
 Db 362 -TFVGHQGPVCLCVYSMGLFSGS 386

RESULT 14

US-10-197-666A-150

; Sequence 150, Application US/1019766A
 ; GENERAL INFORMATION:
 ; APPLICANT: ASAHI KASEI KABUSIKI KAISHA
 ; TITLE OF INVENTION: Etki phosphorylation related gene
 ; FILE REFERENCE: PH-1548US

CURRENT APPLICATION NUMBER: US/10/197,666A
 CURRENT FILING DATE: 2002-11-18

PRIOR APPLICATION NUMBER: JP 2001-218204
 PRIOR FILING DATE: 2001-07-18

PRIOR APPLICATION NUMBER: JP 2001-263450
 PRIOR FILING DATE: 2001-08-31

PRIOR APPLICATION NUMBER: JP 2002-012176
 PRIOR FILING DATE: 2002-01-21

PRIOR APPLICATION NUMBER: US 60/316,304
 PRIOR FILING DATE: 2001-09-04

PRIOR APPLICATION NUMBER: US 60/350,027
 PRIOR FILING DATE: 2002-01-23

NUMBER OF SEQ ID NOS: 156
 SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 150
 LENGTH: 670
 TYPE: PRT
 ORGANISM: Homo sapiens

US-10-197-666A-150

Query Match 6.8%; Score 203; DB 6; Length 670;
 Best Local Similarity 21.5%; Pred. No. 9.7e-11; Mismatches 154; Indels 148; Gaps 18;
 Matches 96; Conservative 48; Mismatches 154; Indels 148; Gaps 18;

Qy 32 VPEQGYKEKVKTVTDKYK-CEKCRVLVCNPQTECCHRFESCMALLSSSSPKCTA 89
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 109 LPEEEEREPPLVFAFSPVSKLCCOLCCSVFKDPVTTGHTFCRRC---ALKSEKCPV 163
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Qy 90 COESIKDKVFKFDCKRELLALQYCRBGRGCAEQJLGHFLVHLNECOP--ELP 146
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 164 ---DN-----VKTIVVNN--IAVAEQ--IGELFIHCRHGCRAVGSGKPP 201
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Qy 147 CLRAD--CKEKVLRKDLRHVKEACKYREATCSHCKSQVPMKLQRHDTPCPVVSC 203
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 202 IFEVPRGCPTTIKSARDH-EGSCDRP-----VRC 233
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Qy 204 PHKCSVOTLRSLSAHLBCBVAAPSTOSFKRGCVFQGTNQOQIKAHEASSAVQHVNLLK 263
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 234 PNPNPSCPPLLRMLNLEAHLKRECFT--KCPHSKGCTPFG-----270
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Qy 264 EWSNSLEKKYSLLONESVKNKTSQSLNQICSEIEFIERQZEMRNNESKTLHQRTD 323
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 271 ---NQTYETHLETFR---EGLAEFLQDTR-FHEMV--303
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Qy 324 SQAEEKLKEELKEIRPRFQNWEEDSMKSVEQSQRNVTLE-SVDKSAQGQARNTGLES 382
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 304 ---ALAOKDQEIA-----FLSMLGKUSEKIDQLEKSLERKEFDVIDENSKLSE 349
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Qy 383 QLSRHQDTLSVHOTRLADMDFRQVLETAASYNGVLTWIKRDYKRRQEAVMGKTSYQ 442
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 350 DLMERRDASMLDELSINARLNMGILGSVDPQQIFKCKG-----390
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Qy 443 PFTYGYFGYKMCARVYLNGDMGKGT 468
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 391 -TFVGHQGPVCLCVYSMGLFSGS 415
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 RESULT 15
 US-10-197-666A-116

US-10-197-666A-116

Query Match 6.7%; Score 202; DB 6; Length 631;
 Best Local Similarity 21.3%; Pred. No. 1.1e-10; Mismatches 174; Indels 152; Gaps 17;
 Matches 101; Conservative 48; Mismatches 174; Indels 152; Gaps 17;

Qy 4 SKKMDAAGTLOPNPLQLQDAGRAGSVLVEPQGGYKEKVKTVTDKYKCEKCHLVLCNPK 63
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 44 TKAADGTGTYKHOHRIPPSSESSTLAVSPRFEEDGEPPLVFAEQPSVSKLCCSVFVKDPV 103
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Qy 64 QTEGGIRPCSMALLSSSSPKCTACOESTIKDKVFKDNCCKREILALQYCRNBSGRG 123
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 104 ITTCGHTFCRC---ALKSEKCPV-----DNA-----KLTVVVNN--IAV 138
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Qy 124 AEQLTGHLTVHLNECOP-----FEELPLRADCKEKEVLRKDJDHYEKAYREA 174
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 139 AEQ--IGELFIHCRHGCRAVGSGKPP 191
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Qy 175 TCSHKSQVPMIKLOKHEDTDCPCVVWSCPHKSQVQLLRSLSLAHSECNAPSTCSFK 234
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 192 -----VRCPNNPSCPPLKMNLEAHLKECHI--KCPHS 223
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Qy 235 RYGCVOFGTNQNIKAHEASSAVQHVNLLKWEWSLKRVSLLONESVEKNKSIOSLHQI 294
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 224 KYGCFPIG-----NQTYETHLETFR---EGLAEFLQDTR-FHEMV--242
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Qy 295 CSFETIEERQKEMRNNESKTLHQRTDLSQAEKELKEIDKETPRFRONWEADSKSSVE 354
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 243 CRF---EGLKELOQSDR-FHEMV----ALQKQDQIA-----FLRSMLG 281
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Qy 355 SLQRVTELE-SVDKSAQGQARNTGLESQSRHDTLSVDIRLADMDFRQVLETASY 413
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 282 KLSBKINGLEKSELKEVDLDENQSKLSEDMIFRDRASMLDELSHINARLNNGLGSY 341
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Qy 414 NGVLTWKIRDYKRKQEAVMGKTSLSQPRPTGYGYKMCARVYLNGDMGKGT 468
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 342 DPQOIFKCKG-----TFVGHQGPVCLCVYSMGLFSGS 376
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Search completed: December 19, 2002, 15:05:20
 Job time : 21 secs

